

GAP of: 0964sid2 check: 7022 from: 1 to: 405

WPDEF Case 0964 Rad23 SEQ ID NO: 2 corn  
Case 0964 Rad23 SEQ ID NO: 2 corn

to: 0964DP32628 check: 3748 from: 1 to: 398

WPDEF Case 0964D Rad23 SwissProt P32628 S. cerevisiae  
Case 0964D Rad23 SwissProt P32628 S. cerevisiae  
P32628. UV excision repai. . .[gi:418413] BLink, Domains, Links  
LOCUS P32628 398 aa linear PLN 15-SEP-2003  
DEFINITION UV excision repair protein RAD23.  
ACCESSION P32628 . . .

Symbol comparison table: /app/gcg/10.2/gcgcore/data/rundata/blosum62.cmp  
CompCheck: 1102

BLOSUM62 amino acid substitution matrix.  
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid  
substitution matrices from protein blocks. Proc. Natl. Acad.  
Sci. USA 89: 10915-10919.

Gap Weight: 8 Average Match: 2.778  
Length Weight: 2 Average Mismatch: -2.248

Quality: 409 Length: 439  
Ratio: 1.028 Gaps: 15  
Percent Similarity: 46.978 Percent Identity: 37.637

Match display thresholds for the alignment(s):  
| = IDENTITY  
: = 2  
. = 1

0964sid2 x 0964DP32628 March 31, 2003 14:22 ..

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      .      .      .      .      .      .      .      .      .      .
1 .MKLNVKTLKGTNFEIEASPDASVADVVKRIIETTQGQSTYRADQQM.LIY 48
  . | | | : : | : : | | : | . ||
1 mvsltfknfkkekvpldlepsntiletk....tklaqsisceesqikliy 46
      .      .      .      .      .      .      .      .      .      .
49 QGKILKDETTLESNGVAENSFLVIMLSKAKASSSGASTATTAKAPATLAQ 98
  ||:|. | . | . : . | |. | . . . | ||
47 sgkvlqdsktvsecglkdgdqvvmvsqkkstktkvteppiapesat... 93
      .      .      .      .      .      .      .      .      .      .
99 PAAPVAPAASVARTPTQAPVATAETAPPSVQPQAAPAATVAATDDADVYS 148
  | .. | | | | | | | | | | | | | | | : |
94 ..tpgrensteaspstdasaapaatapegsqpqeeqtattertesa.... 137
      .      .      .      .      .      .      .      .      .      .
149 QAASNLVFGNNLEQTIQQILDMGGGTWERDTVVRALRAAYNNPERAIDYL 198
  . | | : ||: ||: || : ||: | | | | | | | | | | | | | |
138 .stpgfvvgternetierimemg...ygreeveralraafnnpdraveyl 183
      .      .      .      .      .      .      .      .      .      .
199 YSGIPENVEAQPVARAPAAGQQTNQQAASPAQPAVALPVQPSPASAGPNA 248
  ||||. | | ||| ||. ||. | ||
184 lmgipenl.....rqpepqqt...aaaaeqpstaattaeqpaed.... 220
      .      .      .      .      .      .      .      .      .      .
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249 NPLNLFPGQVPSGGSNPGVVPAGSGALDALRQLP.....QFQALL 289  
 .|| | | .. | . | || | . | . |  
 221 ...dlfaqaaqggnassgal.gttggatdaaqgppgsigltvedllslr 266  
 . . . . .  
 290 QLVQANPQILQPMLQELGKQNPQILRLIQENQAEFLRLVNES..... 331  
 |. | ||: | |: |: : . ||: | | |. :. |.  
 267 qvvsgnpealapllenisarypqlrehimanpevfvsmlleavgdnmqdv 316  
 . . . . .  
 332 PEG.....GPGGNILGQLAAA.VPQ.....TLTVTPEEERAIQRLEG 367  
 || | : |: ||| . | . |||: :|| ||  
 317 megaddmvegedievtgeaaaaglgggegsfqvdytpeddqaisrlce 366  
 . . . . .  
 368 MGFNRELVLLEVFFACNKDEELTANYLL.DHGHEFDDQQQ 405  
 :|| |:|:|:|:|:|.|. | | | |  
 367 lgferdlviqvyfacdkneeeaanilfsdhad..... 398